

IN THE CLAIMS

Please amend the claims as follows:

1-2. (canceled)

3. (previously presented) The method of claim 14, wherein storing variations is performed using a pointer.

4. (currently amended) The method of claim 14, further comprising, before presenting the represented sequence to a user:
identifying, replets that can be used to represent multiple subsequences.

5. (currently amended) The method of claim 14, further comprising, before presenting the reconstructed represented sequence to a user:
segmenting the matching subsequences into multiple parts to account for location-specific variations of the matching subsequences in the sequence data.

6. (currently amended) The method of claim 14, further comprising, before presenting the reconstructed represented sequence to a user:
storing replet information in a replet-information table using a pointer, so that equivalent replet sequences occupy single storage space.

7- 9. (canceled)

10. (currently amended) The method of claim 14, further comprising, before presenting the reconstructed represented sequence to a user:
storing multiple views of the sequence data at multiple levels of abstraction.

11-13. (canceled)

14. (currently amended) A computer system-implemented method for storing and presenting sequence data, comprising:

- i) specifying a set of reptlets for analysis by a computer system;
- ii) for each reptlet in the set, comparing each reptlet by the computer system to a sequence for determining by the computer system a subsequence of the sequence that matches each reptlet, if any;
- iii) generating entries of match-set data structures by the computer system responsive to the comparing, one match-set data structure for each reptlet, a match-set data structure comprising a sequence identification to identify a subsequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a first and second position parameter, the first position parameter denoting a location in the sequence and the second position parameter denoting an offset from the location;
- iv) storing the generated entries of the match-set data structures in a computer readable memory by the computer system;
- v) deleting by the computer system each matching subsequence from the sequence where it is found;
- vi) concatenating by the computer system, in order, unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence;
- vii) the computer system generating a first representation of representing the sequence responsive to the stored backbone sequence and at least a portion of the stored match-set data and presenting the represented sequence to a user of the computer system;

wherein one of the subsequences is matched by a certain plurality of the reptlets and the method further includes:

- viii) the computer system generating or receiving a selection of one of the certain plurality of reptlets, wherein ~~any non-selected one of the certain plurality of reptlets is deemed a redundant reptlet and the representing-generating the first~~

representation in step vii) is responsive to the selected one of the certain plurality of replets but not responsive to any ~~redundant non-selected~~ replet, and wherein the selected one of the replets has a position within the sequence, and wherein after receiving the selection the computer system updates the first and second parameters for any non-selected replet associated with the selected one of the replets, the updating being responsive to the position of the selected one of the replets;

ix) the computer system generating or receiving a selection of ~~one of the replets deemed a redundant replet~~ a replet that was not selected in step viii); and

x) the computer system generating representing and presenting a second representation of the sequence, wherein the representation representing-in step x) is responsive to the one of the replets indicated by the selection in step ix) instead of the one of the replets indicated by the selection in step vii) and wherein the computer system performs the generating representing-in step x) by reference to the first and second parameters for the one of the replets indicated by the selection in step ix), such that the computer system performs the generating representing-in step x) ~~without repeating the generating of using the position parameters performed updated~~ in step ~~viii)~~.

15. (previously presented) The method of claim 14, wherein, prior to presenting the represented sequence to the user, variations are stored in a list data structure comprising a variation identification.

16. (previously presented) The method of claim 15, wherein the list data structure comprises a subsequence character that matches a "don't care" character in a replet that matches the subsequence.

17. (previously presented) The method of claim 16, wherein, prior to presenting the represented sequence to the user, the position of the subsequence character within the subsequence is stored in the list data structure.

18. (previously presented) The method of claim 15, wherein an indirection pointer points to a variation so that variations common to more than one subsequence are not stored more than once.

19. (previously presented) The method of claim 14, wherein a represented sequence presented to the user is in response to a query by the user.

20. (previously presented) The method of claim 19, wherein a query specifies a replet.

21. (previously presented) The method of claim 14, wherein specifying a set of one or more replets comprises adding a new replet to a pre-existing set for which the steps of claim 14 have been performed.

22. (previously presented) The method of claim 14, wherein specifying a set of one or more replets comprises removing a replet from a pre-existing set for which the steps of claim 14 have been performed.

23. (canceled)